

Morteza Sabri

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[Portfolio](#) | [LinkedIn](#) | [Github](#) | [GoogleScholar](#) | [Orcid](#)

PROFESSIONAL SUMMARY

Experienced bioinformatician specializing in bulk and single-cell RNA-Seq analysis—applied to cardiovascular and neurodevelopment research—proficient in R, Shell, and HPC. Developed pipelines accelerating analysis by 80%, identifying novel biomarkers, boosting productivity and reproducibility. Passionate about teaching and solving biological problems through bioinformatics. For more about my background and projects, please see my portfolio: <https://mortezasabri.github.io/>

HIGHLIGHTED AREAS OF EXPERTISE

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- Bulk & single-cell RNA-Seq
 - Data Visualization & Reproducibility
 - R programming & Shell Scripting
 - Study design & Data Interpretation

EXPERIENCE

Scientific Staff, Bioinformatician | RWTH Aachen University, Aachen Jan 2025 – Apr 2025

- Performed single-cell RNA-Seq analysis to study neuron migration in the absence of DNMT1
- Conducted methylation array data analysis on 64 subjects with postpartum depression
- Handled data preprocessing (Parse Bioscience's Trailmaker), statistical analysis, and visualization

Scientific Staff, Bioinformatician | Technical University of Munich, Munich Nov 2023 - Nov 2024

- Conducted bulk and single-cell RNA-Seq analyses for cardiovascular research
- Managed workflows from raw data to functional interpretation and identifying new biomarkers
- Generated publication-ready visualizations illustrating gene-disease associations
- Optimized preprocessing pipelines with R/Shell scripting, reducing runtime up to 80%

Visiting Scientist, Bioinformatician | Helmholtz Munich, Munich Oct 2024 - Nov 2024

- Performed deconvolution analysis to interpret bulk RNA-Seq datasets using BayesPrism R package to elucidate cell-type composition

Instructor & Freelance (part-time), Bioinformatician | Self-Employed, Tehran 2019 – 2023

- Delivered over 10 onsite workshops on R programming, RNA-Seq, and Linux/Shell scripting
- Provided freelance bioinformatics services including RNA-Seq, epigenomics, and visualization
- Supported manuscript revisions by performing advanced statistical analyses (e.g., MINT)
- Hosted Biocast101 podcast ([Apple](#), [Spotify](#), [Castbox](#), [PodLink](#))
- Created contents on social media known as Bioinformatics101 ([YouTube](#), [Instagram](#), etc)

Compulsory Military Service | Department of Defense, Tehran 2020 – 2022

- Sampled blood and oral swabs (COVID-19), performing CBC diagnostics
- Managed patient reception, communication, and scheduling

Research Assistant | National Institute of Genetic Engineering and Biotechnology, Tehran 2019 – 2020

- Produced publication quality visualizations (heatmaps, volcano plots) to support manuscript figures
- Co-authored a peer reviewed article on monolignol biosynthesis in *Camelina sativa*
- Conducted bulk RNA-Seq analyses on *Camelina sativa*

Scientific Researcher | University of Sistan and Baluchestan, Zahedan 2017 – 2019

- Designed and executed qRT-PCR experiments comparing drought responses in two grapevine cultivars
- Performed statistical analyses and produced publication-quality visualizations
- Authored grant proposals on drought-stress gene-expression profiling and medicinal plant genomics
- Lead-authored Master's thesis and manuscript on drought-stress gene expression, overseeing study design, and data interpretation
- Supervised two cohorts of B.Sc. students on *Drosophila melanogaster* genetics projects
- Analyzed publicly available bulk RNA-Seq and miRNA-Seq datasets to identify stress-responsive genes
- Co-authored a peer-reviewed article on trastuzumab resistance in HER2-positive breast cancer

SKILLS

Lab Techniques: RNA/DNA isolation, PCR/qRT-PCR, primer design and optimization, electrophoresis

Programming Languages: R, Python (basic), MATLAB (basic), Shell/Bash, Git/GitHub, LaTeX, Markdown

Bioinformatics Workflows: Bulk RNA-Seq, scRNA-Seq, methylation arrays ([see portfolio for details](#))

Software: CLC Genomics Workbench, Galaxy, SPSS, JupyterLab, Trailmaker

HPC Platforms: Sherlock cluster (Stanford University) and RWTH Aachen cluster

Transferable & Soft Skills: Scientific writing, teaching & mentoring, workshop design & delivery, open science & reproducibility, FAIR data management, teamwork & communication

EDUCATION

M.Sc. Biology (Genetics), University of Sistan and Baluchestan, Iran 2015 – 2019

- **Thesis:** "Investigation of Superoxide Dismutase and Catalase Gene Expression under Drought Stress: A Comparative Study between Sistan and Baluchestan and Moderate Cultivars"

B.Sc. Cellular and Molecular Biology (Genetics), Islamic Azad University, Iran 2011 – 2014

CERTIFICATIONS & LANGUAGES

TOEFL iBT, ETS - Score: 110, February 2023

Languages: Persian (Native), English (Proficient), Azeri (Basic)

PUBLICATION

Overcoming trastuzumab resistance in HER2-positive breast cancer, Journal of Cellular Physiology, 2019
[DOI: 10.1002/jcp.29216](#)

Evaluation of monolignol biosynthesis gene network in Camelina sativa, Agricultural Biotechnology Journal, 2020

Investigation of Superoxide Dismutase and Catalase Gene Expression under Drought Stress: A Comparative Study between Sistan and Baluchestan and Moderate Cultivars – (Manuscript in preparation)

TEACHING EXPERIENCE

Workshops: R & Linux/Shell programming, RNA-Seq, Visualization and basic stats in R
[see portfolio for details](#)

HIGHLIGHTED PIPELINES

- Bulk RNA-Seq (STAR/HISAT2 → DESeq2/edgeR → GO/KEGG)
- scRNA-Seq (Seurat & SingleCellExperiment)
- Genome assembly (Velvet, SPAdes)
- Epigenomic analyses (minfi and limma on IDAT files)

[see portfolio for details](#)

INTERESTS

Genome editing, Machine learning, Comparative genomics, Data science, Computer science, Boulderling, Climbing, Hiking, Camping, Mountaineering

REFERENCE

Prof. Dr. Lars Mägdefessel
Dr. Mahboubeh Yazdanifar
Dr. Komeil Razmi

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